RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/600,997A
Source: IFW16
Date Processed by STIC: 9/28/06

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IFW16

RAW SEQUENCE LISTING DATE: 09/28/2006
PATENT APPLICATION: **US/10/600,997A** TIME: 09:05:34

Input Set : **A:\A-71608 (substitute).ST25.txt**
Output Set: **N:\CRF4\09282006\J600997A.raw**

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 3 <110> APPLICANT: Murphy, Kenneth
 4       Watanabe, Norihiko
 5       Murphy, Theresa
 6       Yang, Jianfei
 8 <120> TITLE OF INVENTION: BTLA Nucleic Acids (amended)
10 <130> FILE REFERENCE: A-71608
12 <140> CURRENT APPLICATION NUMBER: 10/600,997A
13 <141> CURRENT FILING DATE: 2003-06-20
15 <150> PRIOR APPLICATION NUMBER: US 60/390,653
16 <151> PRIOR FILING DATE: 2002-06-20
18 <150> PRIOR APPLICATION NUMBER: US 60/438,593
19 <151> PRIOR FILING DATE: 2003-01-06
21 <160> NUMBER OF SEQ ID NOS: 62
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 283
27 <212> TYPE: PRT
28 <213> ORGANISM: Mus musculus
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37             20                  25                  30
40 Gly Lys His Phe Ile Thr Val Thr Thr Phe Thr Ser Ala Gly Asn Ile
41         35                  40                  45
44 Gly Glu Asp Gly Thr Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
45     50                  55                  60
48 Asn Gly Ile Val Ile Gln Trp Leu Lys Glu Gly Ile Lys Gly Leu Val
49 65                  70                  75                  80
52 His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Gln Gln His Glu Met
53                 85                  90                  95
56 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Val Val Gly Asn
57             100                 105                 110
60 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
61         115                 120                 125
64 Thr Cys Tyr Ile Arg Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
65     130                 135                 140
68 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Ile Asn Val Asp Tyr Asn
69 145                 150                 155                 160
72 Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
73                 165                 170                 175
76 Pro Thr Val Ala Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
77             180                 185                 190
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81         195                 200                 205
84 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
85     210                 215                 220
88 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
89 225                 230                 235                 240
92 Thr Asp Ser Glu Val Lys Arg Arg Ser Gln Leu Gln Leu Leu Asn Ser
93                 245                 250                 255
96 Gly Pro Ser Pro Cys Val Phe Ser Ser Ala Phe Ala Ala Gly Trp Ala
97             260                 265                 270
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101         275                 280
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116             20                  25                  30
119 Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
120         35                  40                  45
123 Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
124     50                  55                  60
127 Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
128 65                  70                  75                  80
131 His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
132                 85                  90                  95
135 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
136             100                 105                 110
139 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
140         115                 120                 125
143 Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
144     130                 135                 140
147 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
148 145                 150                 155                 160
151 Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
152                 165                 170                 175
155 Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
156             180                 185                 190
159 Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
160         195                 200                 205
163 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
164     210                 215                 220
167 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
168 225                 230                 235                 240
171 Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
172                 245                 250                 255
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185 <212> TYPE: DNA
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193 accttcacct cagctggaaa cattggagag gacgggaccc tgagctgcac ttttgaacct 180
195 gacatcaaac tcaacggcat cgtcatccag tggctgaaag aaggcatcaa aggtttggtc 240
197 cacgagttca aagaaggcaa agacgacctc tcacagcagc atgagatgtt cagaggccgc 300
199 acagcagtgt ttgctgatca ggtggtagtt ggcaatgctt ccctgagact gaaaaacgtg 360
201 cagctcacgg atgctggcac ctacacatgt tacatccgca cctcaaaagg caaagggaat 420
203 gcaaacctag agtataagac cggagccttc agtatgccag agataaatgt ggactataat 480
205 gccagttcag agagtttacg ctgcgaggct cctcggtggt tcccccagcc cacagtggcc 540
207 tgggcatctc aagtcgacca aggagccaac ttctcagaag tctcgaacac cagctttgag 600
209 ttgaactctg agaatgtgac catgaaggtc gtatctgtgc tctacaatgt cacaatcaac 660
211 aacacatact cctgtatgat tgaaaatgac attgccaaag ccactgggga catcaaagtg 720
213 acagattcag aggtcaaaag gcggagtcag ctgcagctgc tcaactccgg gccttccccg 780
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221 <211> LENGTH: 849
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 4
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228 ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat cacagtcact 120
230 actgtcgcct cagctgggaa cattggggag gatggaatcc tgagctgcac ttttgaacct 180
232 gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 240
234 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg 300
236 acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg 360
238 caactcacag atgctggcac ctacaaatgt tatatcatca cttctaaagg caaggggaat 420
240 gctaaccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt ggactataat 480
242 gccagctcag agaccttgcg gtgtgaggct ccccgatggt tcccccagcc cacagtggtc 540
244 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac cagctttgag 600
246 ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc tctacaatgt tacgatcaac 660
248 aacacatact cctgtatgat tgaaaatgac attgccaaag caacagggga tatcaaagtg 720
250 acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaaa ggcttctctg 780
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258 <211> LENGTH: 306
259 <212> TYPE: PRT
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268 Phe Phe Ile Leu His Leu Gly Leu Trp Ser Ile Leu Cys Glu Lys Ala
269             20                  25                  30
272 Thr Lys Arg Asn Asp Glu Glu Cys Glu Val Gln Leu Asn Ile Lys Arg
273         35                  40                  45
276 Asn Ser Lys His Ser Ala Trp Thr Gly Glu Leu Phe Lys Ile Glu Cys
277     50                  55                  60
280 Pro Val Lys Tyr Cys Val His Arg Pro Asn Val Thr Trp Cys Lys His
281 65                  70                  75                  80
284 Asn Gly Thr Ile Trp Val Pro Leu Glu Val Gly Pro Gln Leu Tyr Thr
285                 85                  90                  95
288 Ser Trp Glu Glu Asn Arg Ser Val Pro Val Phe Val Leu His Phe Lys
289             100                 105                 110
292 Pro Ile His Leu Ser Asp Asn Gly Ser Tyr Ser Cys Ser Thr Asn Phe
293         115                 120                 125
296 Asn Ser Gln Val Ile Asn Ser His Ser Val Thr Ile His Val Arg Glu
297     130                 135                 140
300 Arg Thr Gln Asn Ser Ser Glu His Pro Leu Ile Thr Val Ser Asp Ile
301 145                 150                 155                 160
304 Pro Asp Ala Thr Asn Ala Ser Gly Pro Ser Thr Met Glu Glu Arg Pro
305                 165                 170                 175
308 Gly Arg Thr Trp Leu Leu Tyr Thr Leu Leu Pro Leu Gly Ala Leu Leu
309             180                 185                 190
312 Leu Leu Leu Ala Cys Val Cys Leu Leu Cys Phe Leu Lys Arg Ile Gln
313         195                 200                 205
316 Gly Lys Glu Lys Lys Pro Ser Asp Leu Ala Gly Arg Asp Thr Asn Leu
317     210                 215                 220
320 Val Asp Ile Pro Ala Ser Ser Arg Thr Asn His Gln Ala Leu Pro Ser
321 225                 230                 235                 240
324 Gly Thr Gly Ile Tyr Asp Asn Asp Pro Trp Ser Ser Met Gln Asp Glu
325                 245                 250                 255
328 Ser Glu Leu Thr Ile Ser Leu Gln Ser Glu Arg Asn Asn Gln Gly Ile
329             260                 265                 270
332 Val Tyr Ala Ser Leu Asn His Cys Val Ile Gly Arg Asn Pro Arg Gln
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345 <211> LENGTH: 289
346 <212> TYPE: PRT
347 <213> ORGANISM: Homo sapiens
349 <400> SEQUENCE: 6
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356             20                  25                  30
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359 Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His Ser Ile
360         35                  40                  45
363 Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala
364     50                  55                  60
367 Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val
368 65                  70                  75                  80
371 Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn Ile Ser
372                 85                  90                  95
375 Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn Gly Ser
376             100                 105                 110
379 Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser
380         115                 120                 125
383 Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser
384     130                 135                 140
387 Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Ser Leu Leu Pro
388 145                 150                 155                 160
391 Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys
392                 165                 170                 175
395 Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala
396             180                 185                 190
399 Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr
400         195                 200                 205
403 Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly
404     210                 215                 220
407 Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser
408 225                 230                 235                 240
411 Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val
412                 245                 250                 255
415 Tyr Ala Ser Leu Asn His Ser Val Ile Gly Leu Asn Ser Arg Leu Ala
416             260                 265                 270
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427 <210> SEQ ID NO: 7
428 <211> LENGTH: 870
429 <212> TYPE: DNA
430 <213> ORGANISM: Homo sapiens
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435 ccatatctgg acatctggaa catccatggg aaagaatcat gtgatgtaca gctttatata    120
437 aagagacaat ctgaacactc catcttagca ggagatccct ttgaactaga atgccctgtg    180
439 aaatactgtg ctaacaggcc tcatgtgact tggtgcaagc tcaatggaac aacatgtgta    240
441 aaacttgaag atagacaaac aagttggaag gaagagaaga acatttcatt tttcattcta    300
443 cattttgaac caatgcttcc taatgacaat gggtcatacc gctgttctgc aaattttcag    360
445 tctaatctca ttgaaagcca ctcaacaact ctttatgtga cagatgtaaa aggtgcctca    420
447 gaacgaccct ccaaggacga agtggcaagc agaccctggc tcctgtatag tttacttcct    480
449 ttgggggat tgcctctact catcactacc tggttctgcc tgttctgctg cctgagaagg    540
451 caccaaggaa agcaaaatga actctctgac acagcaggaa gggaaattaa tctggttgat    600
453 gctcacctta agagcgagca aacagaagca agcaccaggc aaaattccca agtactgcta    660
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VERIFICATION SUMMARY DATE: 09/28/2006
PATENT APPLICATION: **US/10/600,997A** TIME: 09:05:35

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